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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/715,417A

DATE: 01/07/2002

TIME: 11:52:56

Input Set : A:\Cura 606.APP

Output Set: N:\CRF3\01072002\I715417A.raw

ps

<X>

3 <110> APPLICANT: Shimkets, Richard
4 Lichenstein, Henri
5 Vernet, Corine
6 Fernandes, Elma
8 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
10 <130> FILE REFERENCE: 15966-606
12 <140> CURRENT APPLICATION NUMBER: 09/715,417A
13 <141> CURRENT FILING DATE: 2001-11-16

ENTERED

15 <150> PRIOR APPLICATION NUMBER: 60/166,336
16 <151> PRIOR FILING DATE: 1999-11-19
18 <150> PRIOR APPLICATION NUMBER: 60/167,785
19 <151> PRIOR FILING DATE: 1999-11-29
21 <150> PRIOR APPLICATION NUMBER: 60/187,844
22 <151> PRIOR FILING DATE: 2000-03-08
24 <160> NUMBER OF SEQ ID NOS: 38
26 <170> SOFTWARE: PatentIn Ver. 2.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 791
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <400> SEQUENCE: 1

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35 ggtggtattc tgatcacagc tgggtggtat tctgatcaca gctgggtggt attctgatca 120
36 cagctgggtg gtattctgat cacagctggg tggattctg atcacagctg ggtggtattc 180
37 tgatcacagc tgggtggtat tctgatcaca gctgggtggt gatgccaga gtctccattc 240
38 caccctatcc aattgctgga ggagtgtatg acttagatga agacacaccc ccaatagtgt 300
39 cacaatttcc cgggaccatg gctaaacctc ctggatcatt agccagaagc agcagcctgt 360
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41 cacacgcccc ccaccgtca caccctcggc accctcacca cccgcaacac acaccacact 480
42 ccttgcttcc cctgatcca gatattctct cagtgtcaag ttgacctgcy ctttatcgaa 540
43 atgaagagga ggaagaggcc atttacttct ctgctgaaaa gcaatgtatg atcatagtca 600
44 ccagcaagat gcctttactg acagaactgg tcttggtgtg tttctggaaa tcagaaggaa 660
45 aactcgagag ctgcactgtc taataaaact tctgcattg atggaacgtt cagttctcat 720
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47 tggaaaaaaa a 791

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51 <211> LENGTH: 153
52 <212> TYPE: PRT
53 <213> ORGANISM: Homo sapiens
55 <400> SEQUENCE: 2

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57 1 5 10 15
59 Asp Leu Asp Glu Asp Thr Pro Pro Ile Val Ser Gln Phe Pro Gly Thr
60 20 25 30
62 Met Ala Lys Pro Pro Gly Ser Leu Ala Arg Ser Ser Ser Leu Cys Arg
63 35 40 45
65 Ser Arg Arg Ser Ile Val Pro Ser Ser Pro Gln Pro Gln Arg Ala Gln

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66      50      55      60
68 Leu Ala Pro His Ala Pro His Pro Ser His Pro Arg His Pro His His
69 65      70      75      80
71 Pro Gln His Thr Pro His Ser Leu Pro Ser Pro Asp Pro Asp Ile Leu
72      85      90      95
74 Ser Val Ser Ser Cys Pro Ala Leu Tyr Arg Asn Glu Glu Glu Glu Glu
75      100      105      110
77 Ala Ile Tyr Phe Ser Ala Glu Lys Gln Cys Met Ile Ile Val Thr Ser
78      115      120      125
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95 tgggccttgc tcaagccagc aaggggctga atccctgtgt ttcaggactc aggtttgtctg 180
96 agtgtcatca ccgatcccat ccacaccca gtactctct tctggccac cgaccaagcc 240
97 ctccatgccc tacctgctga acaacaggac ttcctgttca accaagacaa caaggacaag 300
98 ctgaaggagt atttgaagtt tcatgtgata cgagatgcca aggttttagc tgtggatctt 360
99 cccacatcca ctgcctggaa gacctgcaa ggttcagagc tgagtgtgaa atgtggagct 420
100 ggcagggaca tcggtgacct ctttctgaat ggccaaacct gcagaattgt gcagcgggag 480
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102 gggggccgct gtgacacctt tactactttc gatgcctcgg gggagtgtgg gagctgtgtc 600
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104 aacctgccct tcaagaggaa cctggaaggc tgccgggagc gatgcagcct ggtgatacag 720
105 atccccaggt gctgcaaggg ctacttcggg cgagactgtc aggcctgccc tggaggacca 780
106 gatgccccgt gtaataaccg ggggtgtctgc cttgatcagt actcgccac cggagagtgt 840
107 aaatgaaca ccggcttcaa tgggacggcg tgtgagatgt gctggccggg gagatttggg 900
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112 aaacaggaca acgggggctg tgcaaagggt gccagatgct cccagaaggg cacgaaggtc 1200
113 tcctgcagct gccagaaggg atacaaaggg gacgggcaca gctgcacaga gatagacccc 1260
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116 gagcagctgc ccattgaccg ctgcttacag gacaatgggc agtgccatgc agacgcaaaa 1440
117 tgtgccgacc tccacttcca ggataccact gttgggggtg tccatctacg ctccccactg 1500
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120 ggctggctgg agaccgggcg ggttgccctac cccacagcct tcgcctccca gaactgtggc 1680
121 tctgggtgtg ttgggatagt ggactatgga cccagaccca acaagagtga aatgtgggat 1740
122 gtcttctgct atcggatgaa aggaagtgtc ggcctattcc aacagctcag ctcgaggccg 1800
123 tgcatttcta gaacacctga ctgacctgtc catccgcggc accctctttg tgccacagaa 1860

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124 cagtgggctg ggggagaatg agaccttgctc tgggcggggac atcgaacacc acctcgccaa 1920
125 tgtcagcatg tttttctaca atgaccttgt caatggcacc accctgcaaa cgaggctggg 1980
126 aagcaagctg ctcactactg ccagccagga c 2011
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130 <211> LENGTH: 315
131 <212> TYPE: PRT
132 <213> ORGANISM: Homo sapiens
134 <400> SEQUENCE: 4
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138 Ser Asp His Gly Gln Cys Asp Asp Gly Ile Thr Gly Ser Gly Gln Cys
139 20 25 30
141 Leu Cys Glu Thr Gly Trp Thr Gly Pro Ser Cys Asp Thr Gln Ala Val
142 35 40 45
144 Leu Ser Ala Val Cys Thr Pro Pro Cys Ser Ala His Ala Thr Cys Lys
145 50 55 60
147 Glu Asn Asn Thr Cys Glu Cys Asn Leu Asp Tyr Glu Gly Asp Gly Ile
148 65 70 75 80
150 Thr Cys Thr Val Val Asp Phe Cys Lys Gln Asp Asn Gly Gly Cys Ala
151 85 90 95
153 Lys Val Ala Arg Cys Ser Gln Lys Gly Thr Lys Val Ser Cys Ser Cys
154 100 105 110
156 Gln Lys Gly Tyr Lys Gly Asp Gly His Ser Cys Thr Glu Ile Asp Pro
157 115 120 125
159 Cys Ala Asp Gly Leu Asn Gly Gly Cys His Glu His Ala Thr Cys Lys
160 130 135 140
162 Met Thr Gly Pro Gly Lys His Lys Cys Glu Cys Lys Ser His Tyr Val
163 145 150 155 160
165 Gly Asp Gly Leu Asn Cys Glu Pro Glu Gln Leu Pro Ile Asp Arg Cys
166 165 170 175
168 Leu Gln Asp Asn Gly Gln Cys His Ala Asp Ala Lys Cys Ala Asp Leu
169 180 185 190
171 His Phe Gln Asp Thr Thr Val Gly Val Phe His Leu Arg Ser Pro Leu
172 195 200 205
174 Gly Gln Tyr Lys Leu Thr Phe Asp Lys Ala Arg Glu Ala Cys Ala Asn
175 210 215 220
177 Glu Ala Ala Thr Met Ala Thr Tyr Asn Gln Leu Ser Tyr Ala Gln Lys
178 225 230 235 240
180 Ala Lys Tyr His Leu Cys Ser Ala Gly Trp Leu Glu Thr Gly Arg Val
181 245 250 255
183 Ala Tyr Pro Thr Ala Phe Ala Ser Gln Asn Cys Gly Ser Gly Val Val
184 260 265 270
186 Gly Ile Val Asp Tyr Gly Pro Arg Pro Asn Lys Ser Glu Met Trp Asp
187 275 280 285
189 Val Phe Cys Tyr Arg Met Lys Gly Ser Ala Gly Leu Phe Gln Gln Leu
190 290 295 300
192 Ser Ser Arg Pro Cys Ile Ser Arg Thr Pro Asp
193 305 310 315
196 <210> SEQ ID NO: 5

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198 <212> TYPE: DNA
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204 tgggccttgc tcaagccagc aaggggctga atccctgtgt ttcaggactc aggtttgtctg 180
205 agtgtcatca ccgatcccat ccacacccca gtcactctct tctggcccac cgaccaagcc 240
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207 ctgaaggagt atttgaagtt tcatgtgata cgagatgcc aagttttagc tgtggatctt 360
208 cccacatcca ctgcctggaa gaccctgcaa gggtcagagc tgagtgtgaa atgtggagct 420
209 ggcagggaca tcggtgacct ctttctgaat ggccaaacct gcagaattgt gcagcgggag 480
210 ctcttgtttg acctgggtgt ggctacggc attgactgtc tgcctgattga tcccaccctg 540
211 gggggccgct gtgacacctt tactactttc gatgcctcgg gggagtgtgg gagctgtgtc 600
212 aatactccca gctgccaag gtggagtaaa ccaaaggggtg tgaagcagaa gtgtctctac 660
213 aacctgcctt tcaagaggaa cctggaaggc tgccgggagc gatgcagcct ggtgatacag 720
214 atccccaggt gctgcaaggg ctacttcggg cgagactgtc aggcctgccc tggaggacca 780
215 gatgccccgt gtaataaccg ggggtgtctg cttgatcagt actcggccac cggagagtgt 840
216 aaatgcaaca ccggcttcaa tgggacggcg tgtgagatgt gctggccggg gagatttggg 900
217 cctgattgtc tgccctgtgg ctgctcagac cacggacagt gcgatgatgg catcacgggc 960
218 tccgggcagt gcctctgtga aacgggggtg acaggccct cgtgtgacac tcaggcagtt 1020
219 ttgtctgcag tgtgtacgcc tccttgttct gctcatgcc cctgtaagga gaacaacacg 1080
220 tgtgagtgtg acctggatta tgaagggtgac ggaatcacat gcacagttgt ggatttctgc 1140
221 aaacaggaca acgggggctg tgcaaagggt gccagatgct cccagaaggg cacgaaggctc 1200
222 tcctgcagct gccagaagg atacaaaggg gacgggcaca gctgcacaga gatagacccc 1260
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225 gagcagctgc ccattgaccg ctgcttacag gacaatgggc agtgccatgc agacgccaaa 1440
226 tgtgtcgacc tccacttcca ggataccact gttgggggtg tccatctacg ctccccactg 1500
227 ggccagtata agctgacctt tgacaaagcc agagaggcct gtgccaacga agctgcgacc 1560
228 atggcaacct acaaccagct ctcctatgcc cagaagagag aagagaaatg agtatgaaag 1620
229 acctgggac ctacaagaaa gagaggacac ttttgttcac ccagtggctc aatcaaccag 1680
230 tcaacatcta atgaccacct actgtgtgcc aggcacagag gtgcaatagg caaagccaag 1740
231 taccacctgt gtcagcagg ctggctggag accgggcggg ttgcctaccc cacagccttc 1800
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236 <211> LENGTH: 244
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238 <213> ORGANISM: Homo sapiens
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245 20 25 30
247 Leu Cys Glu Thr Gly Trp Thr Gly Pro Ser Cys Asp Thr Gln Ala Val
248 35 40 45
250 Leu Ser Ala Val Cys Thr Pro Pro Cys Ser Ala His Ala Thr Cys Lys
251 50 55 60
253 Glu Asn Asn Thr Cys Glu Cys Asn Leu Asp Tyr Glu Gly Asp Gly Ile

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254 65              70              75              80
256 Thr Cys Thr Val Val Asp Phe Cys Lys Gln Asp Asn Gly Gly Cys Ala
257              85              90              95
259 Lys Val Ala Arg Cys Ser Gln Lys Gly Thr Lys Val Ser Cys Ser Cys
260              100              105              110
262 Gln Lys Gly Tyr Lys Gly Asp Gly His Ser Cys Thr Glu Ile Asp Pro
263              115              120              125
265 Cys Ala Asp Gly Leu Asn Gly Gly Cys His Glu His Ala Thr Cys Lys
266              130              135              140
268 Met Thr Gly Pro Gly Lys His Lys Cys Glu Cys Lys Ser His Tyr Val
269 145              150              155              160
271 Gly Asp Gly Leu Asn Cys Glu Pro Glu Gln Leu Pro Ile Asp Arg Cys
272              165              170              175
274 Leu Gln Asp Asn Gly Gln Cys His Ala Asp Ala Lys Cys Val Asp Leu
275              180              185              190
277 His Phe Gln Asp Thr Thr Val Gly Val Phe His Leu Arg Ser Pro Leu
278              195              200              205
280 Gly Gln Tyr Lys Leu Thr Phe Asp Lys Ala Arg Glu Ala Cys Ala Asn
281              210              215              220
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284 225              230              235              240
286 Arg Glu Glu Lys

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291 <211> LENGTH: 1450

292 <212> TYPE: DNA

293 <213> ORGANISM: Homo sapiens

295 <220> FEATURE:

296 <221> NAME/KEY: misc_feature

297 <222> LOCATION: (31)

298 <223> OTHER INFORMATION: wherein n is g or a or t or c

300 <400> SEQUENCE: 7

OK → 301 cggcctgtta tttccttttg cgcgacacgg nctcagctgt tgcgcctttg gcgagtgcac 60

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303 ctacctgccc cgttttccct gtgagttgac ctgctccggg ccgcgggcgc caatggcagg 180

304 ggccgctccg accacggcct tcgggcaggc ggtgatcggc ccgcccggcg cagggaagac 240

305 cagtgactgc ctgggcatga gtgagttcct gcgcgcgctg ggccggcgct tggcggtgtg 300

306 tgaacctgga cccggccaac gaggggctgc cgtacgagtg tgccgtggac gtgggcgagc 360

307 tgggtgggct gggcgacgtg atggacgcgc tgcccttggg ggcccaacgg cggcctgctc 420

308 tactgcatgg agtacctgga agccaacctg gactggctgc gtgccaagct cgacccctc 480

309 cgcggccact acttctctt cgactgccc ggcagggtgg agctctgcac gcatcacggc 540

310 gccttgcgag catcttctcc caaatgggc agtgggacct caggctgact gccgtccacc 600

311 tcgtggattc tcaactactg acagaccctg ccaagttcat ttcagtactg tgtacctccc 660

312 tggccaccat gctgcacgtg gaactgagcc cacatcaacc tcttttccaa gatggacctc 720

313 attgagcatt atgggaagct ggccttcaac ctggactact acacagaggt tctggacctc 780

314 tctacctgc ttgaccacct ggcttctgac cttttcttcc gccactaccg ccagctcaat 840

315 gagaagctag tgcagctcat cgaagactat agccttgtct cctttatccc tctcaacatc 900

316 caggacaagg agagcatcca gcgagtcctt caggctgtgg ataaagccaa tggatactgt 960

317 ttcggagccc aagagcagcg aagcttggaa gccatgatgt ctgccgcaat gggagccgac 1020

318 ttccatttct cttccacact gggcatccag gagaagtacc tggcaccctc gaaccagtca 1080

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:1758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29

L:1798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29

L:2250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33

L:2282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34

L:2324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35

L:2379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36

L:2415 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37

L:2451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38